

# SCORE Search Results Details for Appli

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This page gives you Search Results detail for the Application 10693629 and Search Result us-10-69  
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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:34:25 ; Search time 25.6344 Seconds  
(without alignments)  
559.260 Million cell updates/sec

Title: US-10-693-629-48  
Perfect score: 796  
Sequence: 1 MDLMCKKMKHLWFFLLLVAA.....YFGWFDPWGQGLTVTVSSAS 149

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	687	86.3 147	2	S13519	Ig heavy chain V r
2	606	76.1 146	2	S09710	Ig heavy chain V r
3	600	75.4 155	2	S31511	Ig heavy chain - h
4	597	75.0 140	2	I37782	Ig variable region
5	597	75.0 155	2	S31512	Ig heavy chain - h
6	585.5	73.6 137	2	S31676	Ig heavy chain V r
7	584.5	73.4 139	2	S31586	Ig heavy chain V r
8	574	72.1 124	2	S31684	Ig heavy chain V r

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Listing first 45 summaries

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1: pir1:\*  
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## SUMMARIES

Result No.	Query		DB	ID	Description
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# SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-48.rup.

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:27:58 ; Search time 206.143 Seconds  
(without alignments)  
668.599 Million cell updates/sec

Title: US-10-693-629-48  
Perfect score: 796  
Sequence: 1 MDLMCKKMKHLWFFLLLVAA.....YFGWFDPWGQGTTLTVSSAS 149

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	674	84.7	492	2 Q7Z374_HUMAN	Q7z374 homo sapien
2	603.5	75.8	465	2 Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	602.5	75.7	150	2 O95973_HUMAN	O95973 homo sapien
4	602	75.6	476	2 Q6GMX1_HUMAN	Q6gmx1 homo sapien

# SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-49.rng.

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2006, 23:21:08 ; Search time 435.692 Seconds  
(without alignments)  
7169.205 Million cell updates/sec

Title: US-10-693-629-49  
Perfect score: 448  
Sequence: 1 agatcttaagcaagtgtaac.....aggtggaaatcaaacgtacg 448

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2006, 23:51:15 ; Search time 132.431 Seconds  
(without alignments)  
6329.773 Million cell updates/sec

Title: US-10-693-629-49  
Perfect score: 448  
Sequence: 1 agatcttaagcaagtgtaac.....aggtggaaatcaaacgtacg 448

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	
-----							

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OM protein - protein search, using sw model

# SCORE Search Results Details for Application 10 and Search Result us-10-693-629-50.ra

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:40:49 ; Search time 34.0143 Seconds  
(without alignments)  
334.535 Million cell updates/sec

Title: US-10-693-629-50  
Perfect score: 670  
Sequence: 1 MDMRVPAQLLGLLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	602.5	89.9	236	2	US-09-859-053-30	Sequence 30, Appl
2	569.5	85.0	129	1	US-08-217-918-2	Sequence 2, Appli
3	558.5	83.4	129	2	US-09-019-441A-6	Sequence 6, Appli





# SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-50.rapbm.

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:57:24 ; Search time 113.226 Seconds  
(without alignments)  
531.839 Million cell updates/sec

Title: US-10-693-629-50  
Perfect score: 670  
Sequence: 1 MDMRVPAQLLGLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
-----					

# SCORE Seal

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:34:25 ; Search time 22.3656 Seconds  
(without alignments)  
559.260 Million cell updates/sec

Title: US-10-693-629-50  
Perfect score: 670  
Sequence: 1 MDMRVPAQLLGLLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%					Description
	Query	Match	Length	DB	ID	
No.	Score					
1	614.5	91.7	125	2	S40349	Ig kappa chain V-J
2	596.5	89.0	132	2	S40334	Ig kappa chain - h
3	596	89.0	117	2	S11700	Ig kappa chain pre
4	592.5	88.4	132	2	S38646	Ig kappa chain V r
5	586.5	87.5	128	2	S46372	IG light chain var
6	579.5	86.5	125	2	S40333	Ig kappa chain V-J
7	574.5	85.7	141	2	A49134	Ig kappa chain V-I
8	571.5	85.3	127	2	S11240	Ig kappa chain V r

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:34:25 ; Search time 22.3656 Seconds  
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Sequence: 1 MDMRVPAQLLGLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

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Result No.	Score	%		DB	ID	Description
		Query Match	Length			
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2	596.5	89.0	132	2	S40334	Ig kappa chain - h
3	596	89.0	117	2	S11700	Ig kappa chain pre
4	592.5	88.4	132	2	S38646	Ig kappa chain V r
5	586.5	87.5	128	2	S46372	IG light chain var
6	579.5	86.5	125	2	S40333	Ig kappa chain V-J
7	574.5	85.7	141	2	A49134	Ig kappa chain V-I
8	571.5	85.3	127	2	S11240	Ig kappa chain V r

# SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-50.rup.

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:27:58 ; Search time 179.857 Seconds  
(without alignments)  
668.599 Million cell updates/sec

Title: US-10-693-629-50  
Perfect score: 670  
Sequence: 1 MDMRVPAQLLGLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	601.5	89.8	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien	
3	592.5	88.4	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien	
4	590.5	88.1	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien	